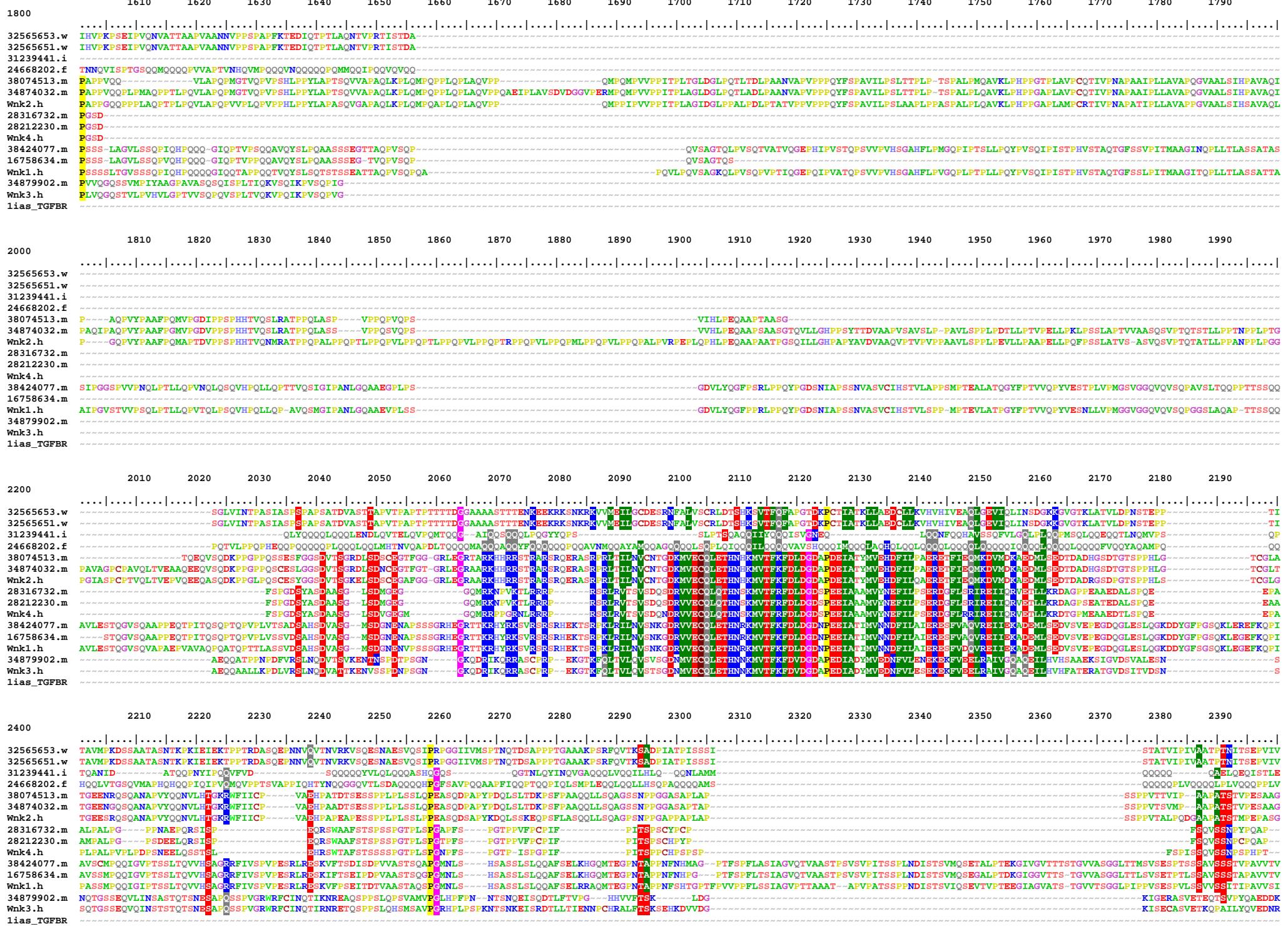


The figure displays sequence alignments for various Wnk genes (Wnk1, Wnk2, Wnk3, and their orthologs) across different species. The top half shows the alignment from position 810 to 990, and the bottom half shows the alignment from position 1410 to 1590. Each sequence is represented by a horizontal bar, with each segment's color corresponding to a specific amino acid. Dashes indicate gaps in the sequence. The alignment highlights regions of high conservation across the different genes and species.



2600

2410 2420 2430 2440 2450 2460 2470 2480 2490 2500 2510 2520 2530 2540 2550 2560 2570 2580 2590

32565653.w QPITAQVITHLAT- PSPVS-HSLSSNS-S-ATTHSNMSSIQS-TTSVPGRRTVQPVSQABSGISS-I-
32565651.w QPITAQVITHLAT- PSEVS-HSLSSNS-S-ATTHSNMSSIQS-TTSVPGRRTVQPVSQABSGISS-I-
31239441.i QQLQG-
24668202.f QQQPLVHQQPS- VQHQQPLVQQPQQQFQPQNQQQPQTQTHVQQPPQQPAVEQI-
38074513.m TAMQAGGGPTGHQG- PASVHETLQPLAETRS-QTALPSTQGQFCPTFALEASRCSTLGEPIS-TREVSQGPQPLITVCAISLAAPD-
34874032.m TAMQAGGGPTGHQG- PASVHETLQPLAETRAGQALPQGQCPCTFALEASHCSTLGEPIS-TKEVSPQGGLTGA-
Wnk2.h TASQAGGGPTPGQ- LTSELETSQPLAETHES-
28316732.m SSSLPLSS-A-SVPLPS-
28212230.m SSSLPLSS-A-SVFFPS-
Wnk4.h SSPLPFSS-S-TEFPVPLSQC-
38424077.m STPSQPVQASTSG- SIASSTGSFPPTFTTTAMGSVVA-
16758634.m STTSQPVQASTSG- SIASSTGSFPPTFTTTGTVSVAVPNAKPP-
Wnk1.h STTPSLOVHTSTSEIVVSSATLYP-
34879902.m -LKA-
Wnk3.h QIMAPVINSSYS-
lias_TGFBR

2800

2610 2620 2630 2640 2650 2660 2670 2680 2690 2700 2710 2720 2730 2740 2750 2760 2770 2780 2790

32565653.w LVIDDHSSDLTQLDSELKRVSGVSHSASP-
32565651.w LVIDDHSSDLTQLDSELKRVSGVSHSASP-
31239441.i VINC-
24668202.f VINCHMENKLKTIKFKDIGDRDETA-
38074513.m RTELYQEVETSSA-SAGTPMEAS-
Wnk2.h RTLYQEVETSSA-SAGTPVEVG-
28316732.m PSPLPS-
28212230.m PPLPS-
Wnk4.h SSFPS-
38424077.m ALL-NQPHTCPEMDADTQS-KAPGIDDIK-
16758634.m ALL-NQPHTCPEMDADTQS-KAPGIDDIK-
Wnk1.h ALL-NQPHTCPEVDSTQ-KAPGIDDIK-
34879902.m RNLLYQEHSSISTICPES-QKDTSIDS-
Wnk3.h RNLLYQEHSSISIYIPES-QKDTSIDS-
lias_TGFBR

3000

2810 2820 2830 2840 2850 2860 2870 2880 2890 2900 2910 2920 2930 2940 2950 2960 2970 2980 2990

32565653.w LGKVIHADGRETTMPDPHD-LDT-
32565651.w LGKVIHADGRETTMPDPHD-LDT-
31239441.i -
24668202.f LLE-SAGNGAPRSNLNPLNRHLKIQEDLKHTRLDDLTAVKTFDMPNKAALDTSENQ-
38074513.m AGC-
34874032.m TGS-
Wnk2.h GRO-
28316732.m PG-
28212230.m PG-
Wnk4.h PSPLPSLPPPVPAGQKESPS-
38424077.m AGT-
16758634.m AGT-
Wnk1.h AGT-
34879902.m RSA-
Wnk3.h RSA-
lias_TGFBR

3200

3010 3020 3030 3040 3050 3060 3070 3080 3090 3100 3110 3120 3130 3140 3150 3160 3170 3180 3190

32565653.w GQMDLES-
32565651.w GQMDLES-
31239441.i -
24668202.f NPDPIPTEASVGITIATGHEKQLSKQPSLEKPSATS-
38074513.m SSIEVGVEP-PASSD-
34874032.m SSIEVGVEP-PASSD-
Wnk2.h SSIEVGVEP-VSSD-
28316732.m SLK-
28212230.m SLK-
Wnk4.h SPK-
38424077.m LKKEGPVITS-PFRD-
16758634.m LKKEGPVITS-PFRD-
Wnk1.h TKKKEGPVAPSPFMDL-GAVI-
34879902.m SSVTTEKNV-EETSTG-
Wnk3.h SSVTPEKEFEETSA-
lias_TGFBR

